

RAW SEQUENCE LISTING
PATENT APPLICATION US/10/023,096

DATE: 05/02/2002
TIME: 15:04:33

INPUT SET: S36842.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: Kruzel, Marian L.
Kurecki, Tomasz
Gollnick, Paul D.
Doyle, Darrell J.

ENTERED

(ii) TITLE OF INVENTION: Cloning, Expression, and Uses of Human
Lactoferrin

(iii) NUMBER OF SEQUENCES: 8

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Jacobson, Price, Holman & Stern
(B) STREET: 400 Seventh St. N.W.
(C) CITY: Washington D.C.
(E) COUNTRY: U.S.A.
(F) ZIP: 20004

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 10/023,096
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US/08/724,586
(B) FILING DATE: 30-SEPT-1996
(A) APPLICATION NUMBER: US 08/238,445
(B) FILING DATE: 05-MAY-1994

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Player, William E.
(B) REGISTRATION NUMBER: 31,409
(C) REFERENCE/DOCKET NUMBER: 10505/P58185C

(ix) TELECOMMUNICATION INFORMATION:

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47      (A) TELEPHONE: (202) 638-6666
48      (B) TELEFAX: (202) 393-5350
49
50
51      (2) INFORMATION FOR SEQ ID NO:1:
52
53          (i) SEQUENCE CHARACTERISTICS:
54              (A) LENGTH: 2086 base pairs
55              (B) TYPE: nucleic acid
56              (C) STRANDEDNESS: single
57              (D) TOPOLOGY: linear
58
59          (ii) MOLECULE TYPE: DNA (genomic)
60
61          (iii) HYPOTHETICAL: NO
62
63          (iv) ANTI-SENSE: NO
64
65
66          (ix) FEATURE:
67              (A) NAME/KEY: CDS
68              (B) LOCATION: 1..2086
69
70
71          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
72
73      GGA TCC GGC CGT AGG AGA AGG AGT GTT CAG TGG TGC GCC GTA TCC CAA      48
74      Gly Ser Gly Arg Arg Arg Ser Val Gln Trp Cys Ala Val Ser Gln
75      1          5          10          15
76
77      CCC GAG GCC ACA AAA TGC TTC CAA TGG CAA AGG AAT ATG AGA AAA GTG      96
78      Pro Glu Ala Thr Lys Cys Phe Gln Trp Gln Arg Asn Met Arg Lys Val
79      20          25          30
80
81      CGT GGC CCT CCT GTC AGC TGC ATA AAG AGA GAC TCC CCC ATC CAG TGT      144
82      Arg Gly Pro Pro Val Ser Cys Ile Lys Arg Asp Ser Pro Ile Gln Cys
83      35          40          45
84
85      ATC CAG GCC ATT GCG GAA AAC AGG GCC GAT GCT GTG ACC CTT GAT GGT      192
86      Ile Gln Ala Ile Ala Glu Asn Arg Ala Asp Ala Val Thr Leu Asp Gly
87      50          55          60
88
89      GGT TTC ATA TAC GAG GCA GGC CTG GCC CCC TAC AAA CTG CGA CCT GTA      240
90      Gly Phe Ile Tyr Glu Ala Gly Leu Ala Pro Tyr Lys Leu Arg Pro Val
91      65          70          75          80
92
93      GCG GCG GAA GTC TAC GGG ACC GAA AGA CAG CCA CGA ACT CAC TAT TAT      288
94      Ala Ala Glu Val Tyr Gly Thr Glu Arg Gln Pro Arg Thr His Tyr Tyr
95      85          90          95
96
97      GCC GTG GCT GTG GTG AAG AAG GGC GGC AGC TTT CAG CTG AAC GAA CTG      336
98      Ala Val Ala Val Val Lys Lys Gly Gly Ser Phe Gln Leu Asn Glu Leu
99      100          105          110

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100																	
101	CAA	GGT	CTG	AAG	TCC	TGC	CAC	ACA	GGC	CTT	CGC	AGG	ACC	GCT	GGA	TGG	384
102	Gln	Gly	Leu	Lys	Ser	Cys	His	Thr	Gly	Leu	Arg	Arg	Thr	Ala	Gly	Trp	
103			115					120					125				
104																	
105	AAT	GTC	CCT	ATA	GGG	ACA	CTT	CGT	CCA	TTC	TTG	AAT	TGG	ACG	GGT	CCA	432
106	Asn	Val	Pro	Ile	Gly	Thr	Leu	Arg	Pro	Phe	Leu	Asn	Trp	Thr	Gly	Pro	
107		130					135					140					
108																	
109	CCT	GAG	CCC	ATT	GAG	GCA	GCT	GTG	GCC	AGG	TTC	TTC	TCA	GCC	AGC	TGT	480
110	Pro	Glu	Pro	Ile	Glu	Ala	Ala	Val	Ala	Arg	Phe	Phe	Ser	Ala	Ser	Cys	
111	145					150					155					160	
112																	
113	GTT	CCC	GGT	GCA	GAT	AAA	GGA	CAG	TTC	CCC	AAC	CTG	TGT	CGC	CTG	TGT	528
114	Val	Pro	Gly	Ala	Asp	Lys	Gly	Gln	Phe	Pro	Asn	Leu	Cys	Arg	Leu	Cys	
115					165				170						175		
116																	
117	GCG	GGG	ACA	GGG	GAA	AAC	AAA	TGT	GCC	TTC	TCC	TCC	CAG	GAA	CCG	TAC	576
118	Ala	Gly	Thr	Gly	Glu	Asn	Lys	Cys	Ala	Phe	Ser	Ser	Gln	Glu	Pro	Tyr	
119				180					185					190			
120																	
121	TTC	AGC	TAC	TCT	GGT	GCC	TTC	AAG	TGT	CTG	AGA	GAC	GGG	GCT	GGA	GAC	624
122	Phe	Ser	Tyr	Ser	Gly	Ala	Phe	Lys	Cys	Leu	Arg	Asp	Gly	Ala	Gly	Asp	
123			195					200					205				
124																	
125	GTG	GCT	TTT	ATC	AGA	GAG	AGC	ACA	GTG	TTT	GAG	GAC	CTG	TCA	GAC	GAG	672
126	Val	Ala	Phe	Ile	Arg	Glu	Ser	Thr	Val	Phe	Glu	Asp	Leu	Ser	Asp	Glu	
127		210					215					220					
128																	
129	GCT	GAA	AGG	GAC	GAG	TAT	GAG	TTA	CTC	TGC	CCA	GAC	AAC	ACT	CGG	AAG	720
130	Ala	Glu	Arg	Asp	Glu	Tyr	Glu	Leu	Leu	Cys	Pro	Asp	Asn	Thr	Arg	Lys	
131	225					230					235					240	
132																	
133	CCA	GTG	GAC	AAG	TTC	AAA	GAC	TGC	CAT	CTG	GCC	CGG	GTC	CCT	TCT	CAT	768
134	Pro	Val	Asp	Lys	Phe	Lys	Asp	Cys	His	Leu	Ala	Arg	Val	Pro	Ser	His	
135				245						250					255		
136																	
137	GCC	GTT	GTG	GCA	CGA	AGT	GTG	AAT	GGC	AAG	GAG	GAT	GCC	ATC	TGG	AAT	816
138	Ala	Val	Val	Ala	Arg	Ser	Val	Asn	Gly	Lys	Glu	Asp	Ala	Ile	Trp	Asn	
139				260													

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153	CTG TAC CTT GGC TCC GGC TAC TTC ACT GCC ATC CAG AAC TTG AGG AAA	1008
154	Leu Tyr Leu Gly Ser Gly Tyr Phe Thr Ala Ile Gln Asn Leu Arg Lys	
155	325 330 335	
156		
157	AGT GAG GAG GAA GTG GCT GCC CGG CGT GCG CGG GTC GTG TGG TGT GCG	1056
158	Ser Glu Glu Glu Val Ala Ala Arg Arg Ala Arg Val Val Trp Cys Ala	
159	340 345 350	
160		
161	GTG GGC GAG CAG GAG CTG CGC AAG TGT AAC CAG TGG AGT GGC TTG AGC	1104
162	Val Gly Glu Gln Glu Leu Arg Lys Cys Asn Gln Trp Ser Gly Leu Ser	
163	355 360 365	
164		
165	GAA GGC AGC GTG ACC TGC TCC TCG GCC TCC ACC ACA GAG GAC TGC ATC	1152
166	Glu Gly Ser Val Thr Cys Ser Ser Ala Ser Thr Thr Glu Asp Cys Ile	
167	370 375 380	
168		
169	GCC CTG GTG CTG AAA GGA GAA GCT GAT GCC ATG AGT TTG GAT GGA GGA	1200
170	Ala Leu Val Leu Lys Gly Glu Ala Asp Ala Met Ser Leu Asp Gly Gly	
171	385 390 395 400	
172		
173	TAT GTG TAC ACT GCA GGC AAA TGT GGT TTG GTG CCT GTC CTG GCA GAG	1248
174	Tyr Val Tyr Thr Ala Gly Lys Cys Gly Leu Val Pro Val Leu Ala Glu	
175	405 410 415	
176		
177	AAC TAC AAA TCC CAA CAA AGC AGT GAC CCT GAT CCT AAC TGT GTG GAT	1296
178	Asn Tyr Lys Ser Gln Gln Ser Ser Asp Pro Asp Pro Asn Cys Val Asp	
179	420 425 430	
180		
181	AGA CCT GTG GAA GGA TAT CTT GCT GTG GCG GTG GTT AGG AGA TCA GAC	1344
182	Arg Pro Val Glu Gly Tyr Leu Ala Val Ala Val Val Arg Arg Ser Asp	
183	435 440 445	
184		
185	ACT AGC CTT ACC TGG AAC TCT GTG AAA GGC AAG AAG TCC TGC CAC ACC	1392
186	Thr Ser Leu Thr Trp Asn Ser Val Lys Gly Lys Lys Ser Cys His Thr	
187	450 455 460	
188		
189	GCC GTG GAC AGG ACT GCA GGC TGG AAT ATC CCC ATG GGC CTG CTC TTC	1440
190	Ala Val Asp Arg Thr Ala Gly Trp Asn Ile Pro Met Gly Leu Leu Phe	
191	465 470 475 480	
192		
193	AAC CAG ACG GGC TCC TGC AAA TTT GAT GAA TAT TTC AGT CAA AGC TGT	1488
194	Asn Gln Thr Gly Ser Cys Lys Phe Asp Glu Tyr Phe Ser Gln Ser Cys	
195	485 490 495	
196		
197	GCC CCT GGG TCT GAC CCG AGA TCT AAT CTC TGT GCT CTG TGT ATT GGC	1536
198	Ala Pro Gly Ser Asp Pro Arg Ser Asn Leu Cys Ala Leu Cys Ile Gly	
199	500 505 510	
200		
201	GAC GAG CAG GGT GAG AAT AAG TGC GTG CCC AAC AGC AAC GAG AGA TAC	1584
202	Asp Glu Gln Gly Glu Asn Lys Cys Val Pro Asn Ser Asn Glu Arg Tyr	
203	515 520 525	
204		
205	TAC GGC TAC ACT GGG GCT TTC CGG TGC CTG GCT GAG AAT GCT GGA GAC	1632

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206 Tyr Gly Tyr Thr Gly Ala Phe Arg Cys Leu Ala Glu Asn Ala Gly Asp
207      530                      535                      540
208
209 GTT GCA TTT GTG AAA GAT GTC ACT GTC TTG CAG AAC ACT GAT GGA AAT      1680
210 Val Ala Phe Val Lys Asp Val Thr Val Leu Gln Asn Thr Asp Gly Asn
211 545                      550                      555                      560
212
213 AAC AAT GAG GCA TGG GCT AAG GAT TTG AAG CTG GCA GAC TTT GCG CTG      1728
214 Asn Asn Glu Ala Trp Ala Lys Asp Leu Lys Leu Ala Asp Phe Ala Leu
215                      565                      570                      575
216
217 CTG TGC CTC GAT GGC AAA CGG AAG CCT GTG ACT GAG GCT AGA AGC TGC      1776
218 Leu Cys Leu Asp Gly Lys Arg Lys Pro Val Thr Glu Ala Arg Ser Cys
219                      580                      585                      590
220
221 CAT CTT GCC ATG GCC CCG AAT CAT GCC GTG GTG TCT CGG ATG GAT AAG      1824
222 His Leu Ala Met Ala Pro Asn His Ala Val Val Ser Arg Met Asp Lys
223                      595                      600                      605
224
225 GTG GAA CGC CTG AAA CAG GTG TTG CTC CAC CAA CAG GCT AAA TTT GGG      1872
226 Val Glu Arg Leu Lys Gln Val Leu Leu His Gln Gln Ala Lys Phe Gly
227      610                      615                      620
228
229 AGA AAT GGA TCT GAC TGC CCG GAC AAG TTT TGC TTA TTC CAG TCT GAA      1920
230 Arg Asn Gly Ser Asp Cys Pro Asp Lys Phe Cys Leu Phe Gln Ser Glu
231 625                      630                      635                      640
232
233 ACC AAA AAC CTT CTG TTC AAT GAC AAC ACT GAG TGT CTG GCC AGA CTC      1968
234 Thr Lys Asn Leu Leu Phe Asn Asp Asn Thr Glu Cys Leu Ala Arg Leu
235                      645                      650                      655
236
237 CAT GGC AAA ACA ACA TAT GAA AAA TAT TTG GGA CCA CAG TAT GTC GCA      2016
238 His Gly Lys Thr Thr Tyr Glu Lys Tyr Leu Gly Pro Gln Tyr Val Ala
239                      660                      665                      670
240
241 GGC ATT ACT AAT CTG AAA AAG TGC TCA ACC TCC CCC CTC CTG GAA GCC      2064
242 Gly Ile Thr Asn Leu Lys Lys Cys Ser Thr Ser Pro Leu Leu Glu Ala
243      675                      680                      685
244
245 TGT GAA TTC CTC AGG AAG TAA A      2086
246 Cys Glu Phe Leu Arg Lys *
247      690                      695
248
249

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 694 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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SEQUENCE VERIFICATION REPORT
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Error

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SEQUENCE MISSING ITEM REPORT
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STATE

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SEQUENCE CORRECTION REPORT
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Original Text

Corrected Text